What is Claimed is:

1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on at least one copy of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

HAPLOTYPE NUMBER[a]										PS[b]	PS
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	G	G	G	2	3409
A	A	A	A	A	A	A	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
A	A	A	A	A	A	A	G	G	G	5	4054
G	G	G	G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	A	G	G	8	12356
T	T	T	T	T	T	T	T	C	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	C	C	C	C	C	C	C	C	11	12653
A	G	G	G	G	G	G	G	G	G	12	14824
A	A	A	A	A	G	G	G	A	A	13	14990
C	C	C	C	T	C	C	C	C	C	14	15089
C	C	C	T	C	C	C	C	C	C	15	15093
C	C	T	C	C	C	T	T	T	C	16	15529
G	G	G	G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]										PS[b]	PS
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	T	T	T	2	3409
A	A	A	A	G	G	G	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
G	G	G	G	A	A	A	A	A	A	5	4054
G	G	G	G	G	G	G	A	G	G	6	4082
C	C	C	T	C	C	T	C	C	C	7	11998
G	G	G	G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	T	T	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	T	C	C	C	C	T	C	C	11	12653
G	G	G	G	G	G	G	G	G	G	12	14824
A	G	A	G	A	A	A	A	A	G	13	14990
C	C	C	C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	C	C	C	15	15093
T	T	T	T	C	T	C	T	T	T	16	15529
G	G	G	G	G	G	G	G	A	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]							PS[b]	PS
21	22	23	24	25	26	27	NUMBER	POSITION[c]
G	G	G	G	G	G	T	1	3102
T	T	T	T	T	T	G	2	3409
A	A	A	A	A	G	G	3	3438
C	C	C	C	G	C	C	4	3603
A	A	A	G	A	A	A	5	4054
G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	9	12397
C	C	T	C	C	C	C	10	12489
T	T	T	T	T	C	C	11	12653
G	G	G	G	G	G	G	12	14824
A	A	A	A	A	A	A	13	14990
C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	15	15093
C	T	T	T	T	C	T	16	15529
G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	A	18	16165

[a]Alleles for haplotypes are presented 5′ to 3′ in each column
[b]PS = polymorphic site;
[c]Position of PS within SEQ ID NO:1.

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS18 on both copies of the individual's TNFRSF1A gene, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

HAPLOTYPE PAIR[a]								PS[b]	PS
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/19	3/14	12/15	22/8	2/9	3/21	2/15	12/17	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A	A/A	A/G	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	G/A	A/G	A/G	A/A	A/A	G/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/T	7	11998
G/G	G/G	G/G	G/A	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	C/C	C/C	T/C	C/C	C/T	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	12	14824
A/A	A/G	G/A	A/G	A/A	A/A	A/A	G/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/T	T/T	T/C	T/T	C/T	T/C	C/C	T/C	16	15529
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION[c]
G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/G	G/G	G/T	T/G	G/G	T/G	T/T	2	3409
A/G	A/A	A/G	A/G	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	A/A	A/A	A/G	G/A	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	T/C	C/C	C/C	T/C	C/C	T/C	T/T	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	A/A	A/A	G/G	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/C	C/T	C/C	T/T	T/T	T/C	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]						PS[b]	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

[a]Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1.

3. A method for genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, comprising determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the one or more PS have the position and alternative alleles shown in SEQ ID NO:1.

4. The method of claim 3, wherein the determining step comprises:

(a) isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF1A gene, or a fragment thereof, that are present in the individual;

(b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;

(c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;

(d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

(e) detecting the presence and identity of the terminator in the extended oligonucleotide.

5. The method of claim 3, which comprises determining for the two copies of the TNFRSF1A gene present in the individual the identity of the nucleotide pair at each of PS1-PS18.

6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual which comprises determining, for one copy of the TNFRSF1A gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

7. The method of claim 6, further comprising determining the identity of the nucleotide at one or more polymorphic sites selected from the group consisting of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, which has the location and alternative alleles shown in SEQ ID NO: 1.

8. The method of claim 6, wherein the determining step comprises:

(a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF1A gene, or a fragment thereof, that is present in the individual;

(b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;

(c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in the target region;

(d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

(e) detecting the presence and identity of the terminator in the extended oligonucleotide.

9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual comprising:

(a) identifying a TNFRSF1A genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;

(b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and

(c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

HAPLOTYPE PAIR[a]								PS[b]	PS
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/19	3/14	12/15	22/8	2/9	3/21	2/15	12/17	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A	A/A	A/G	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	G/A	A/G	A/G	A/A	A/A	G/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/T	7	11998
G/G	G/G	G/G	G/A	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	C/C	C/C	T/C	C/C	C/T	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/G	G/A	A/G	A/A	A/A	A/A	G/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/T	T/T	T/C	T/T	C/T	T/C	C/C	T/C	16	15529
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION[c]
G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/G	G/G	G/T	T/G	G/G	T/G	T/T	2	3409
A/G	A/A	A/G	A/G	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	A/A	A/A	A/G	G/A	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	T/C	C/C	C/C	T/C	C/C	T/C	T/T	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	A/A	A/A	G/G	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/C	C/T	C/C	T/T	T/T	T/C	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]						PS[b]	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

[a]Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1.

10. The method of claim 9, wherein the identified genotype of the individual comprises the nucleotide pair at each of PS1-PS18, which have the position and alternative alleles shown in SEQ ID NO:1.

11. A method for identifying an association between a trait and at least one haplotype or haplotype pair of the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-27 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

HAPLOTYPE NUMBER[a]										PS[b]	PS
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	G	G	G	2	3409
A	A	A	A	A	A	A	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
A	A	A	A	A	A	A	G	G	G	5	4054
G	G	G	G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	A	G	G	8	12356
T	T	T	T	T	T	T	T	C	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	C	C	C	C	C	C	C	C	11	12653
A	G	G	G	G	G	G	G	G	G	12	14824
A	A	A	A	A	G	G	G	A	A	13	14990
C	C	C	C	T	C	C	C	C	C	14	15089
C	C	C	T	C	C	C	C	C	C	15	15093
C	C	T	C	C	C	T	T	T	C	16	15529
G	G	G	G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]										PS[b]	PS
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	T	T	T	2	3409
A	A	A	A	G	G	G	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
G	G	G	G	A	A	A	A	A	A	5	4054
G	G	G	G	G	G	G	A	G	G	6	4082
C	C	C	T	C	C	T	C	C	C	7	11998
G	G	G	G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	T	T	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	T	C	C	C	C	T	C	C	11	12653
G	G	G	G	G	G	G	G	G	G	12	14824
A	G	A	G	A	A	A	A	A	G	13	14990
C	C	C	C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	C	C	C	15	15093
T	T	T	T	C	T	C	T	T	T	16	15529
G	G	G	G	G	G	G	G	A	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

	HAPLOTYPE NUMBER[a]							PS[b]	PS
	21	22	23	24	25	26	27	NUMBER	POSITION[c]
	G	G	G	G	G	G	T	1	3102
	T	T	T	T	T	T	G	2	3409
	A	A	A	A	A	G	G	3	3438
	C	C	C	C	G	C	C	4	3603
	A	A	A	G	A	A	A	5	4054
	G	G	G	G	G	G	G	6	4082
	C	C	C	C	C	C	C	7	11998
	G	G	G	G	G	G	G	8	12356
	T	T	T	T	T	T	T	9	12397
	C	C	T	C	C	C	C	10	12489
	T	T	T	T	T	C	C	11	12653
	G	G	G	G	G	G	G	12	14824
	A	A	A	A	A	A	A	13	14990
	C	C	C	C	C	C	C	14	15089
	C	C	C	C	C	C	C	15	15093
	C	T	T	T	T	C	T	16	15529
	G	G	G	G	G	G	G	17	15932
	G	G	G	G	G	G	A	18	16165

[a]Alleles for haplotypes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

HAPLOTYPE PAIR[a]								PS[b]	PS
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/19	3/14	12/15	22/8	2/9	3/21	2/15	12/17	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A	A/A	A/G	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	G/A	A/G	A/G	A/A	A/A	G/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/T	7	11998
G/G	G/G	G/G	G/A	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	C/C	C/C	T/C	C/C	C/T	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	12	14824
A/A	A/G	G/A	A/G	A/A	A/A	A/A	G/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/T	T/T	T/C	T/T	C/T	T/C	C/C	T/C	16	15529
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION[c]
G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/G	G/G	G/T	T/G	G/G	T/G	T/T	2	3409
A/G	A/A	A/G	A/G	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	A/A	A/A	A/G	G/A	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	T/C	C/C	C/C	T/C	C/C	T/C	T/T	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	A/A	A/A	G/G	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/C	C/T	C/C	T/T	T/T	T/C	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]						PS[b]	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

[a]Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

12. The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF1A.

13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS4, PS12, PS14, PS15, PS17 and PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF1A gene at a region containing the polymorphic site.

15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-10, the complements of SEQ ID NOS:4-10, and SEQ ID NOS:11-24.

16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.

17. The primer-extension oligonucleotide of claim 16,which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:25-38.

18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS4, PS12, PS14, PS15, PS17 and

PS18, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

19. The kit of claim 18, which further comprises oligonucleotides designed to genotype each of PS2, PS3, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS13 and PS16, having the location and alternative alleles shown in SEQ ID NO:1.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the TNFRSF1A isogene is selected from the group consisting of isogenes 1-27 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
A	A	A	A	A	A	A	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
A	A	A	A	A	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	C	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	C	C	C	C	C	C	C	C	11	12653	1	11417-12926
A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	G	G	G	A	A	13	14990	1	14634-16768
C	C	C	C	T	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	T	C	C	C	C	C	C	15	15093	1	14634-16768
C	C	T	C	C	C	T	T	T	C	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	T	T	T	2	3409	1	2920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
G	G	G	G	A	A	A	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	A	G	G	6	4082	1	2920-4210
C	C	C	T	C	C	T	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	T	C	C	C	C	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	G	A	G	A	A	A	A	A	G	13	14990	1	14634-16768
C	C	C	C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	C	C	C	15	15093	1	14634-16768
T	T	T	T	C	T	C	T	T	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]							PS[b]	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	T	1	3102	1	2920-4210
T	T	T	T	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	C	C	C	G	C	C	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	T	T	C	C	11	12653	1	11417-12926
G	G	G	G	A	A	A	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	15	15093	1	14634-16768
C	T	T	T	T	C	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

[a]Alleles for isogenes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;
[d]Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.

22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 20, wherein the organism expresses a TNFRSF1A protein that is encoded by the first nucleotide sequence.

23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the selected polymorphism has the position set forth in the table immediately below:

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
A	A	A	A	A	A	A	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
A	A	A	A	A	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	C	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	C	C	C	C	C	C	C	C	11	12653	1	11417-12926
A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	G	G	G	A	A	13	14990	1	14634-16768
C	C	C	C	T	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	T	C	C	C	C	C	C	15	15093	1	14634-16768
C	C	T	C	C	C	T	T	T	C	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	T	T	T	2	3409	1	2920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
G	G	G	G	A	A	A	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	A	G	G	6	4082	1	2920-4210
C	C	C	T	C	C	T	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	T	C	C	C	C	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	G	A	G	A	A	A	A	A	G	13	14990	1	14634-16768
C	C	C	C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	C	C	C	15	15093	1	14634-16768
T	T	T	T	C	T	C	T	T	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]							PS[b]	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	T	1	3102	1	2920-4210
T	T	T	T	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	C	C	C	G	C	C	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	T	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	15	15093	1	14634-16768
C	T	T	T	T	C	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

[a]Alleles for isogenes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;
[d]Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and wherein each of the coding sequences comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isogene Coding Sequence Number				PS	PS
8	9	14,17	19	Number	Position
C	C	T	C	7	224
A	G	G	G	8	362
T	C	T	T	9	403
G	G	G	A	17	935

[a]Alleles for the isogene coding sequence are presented 5′ to 3′ in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:2.

26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein that is encoded by the polymorphic variant sequence.

27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.

28. An isolated fragment of a TNFRSF1A cDNA, wherein the fragment comprises adenine at a

position corresponding to nucleotide 935 in SEQ ID NO:2.

29 An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises lysine at a position corresponding to amino acid position 312.

30. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.

31. A method for screening for drugs targeting the isolated polypeptide of claim 31 which comprises contacting the TNFRSF1A polymorphic variant with a candidate agent and assaying for binding activity.

32. An isolated fragment of the TNFRSF1A polypeptide, wherein the fragment comprises lysine at a position corresponding to amino acid position 312 in SEQ ID NO:3.

33 A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 1A gene, comprising:

(a) a central processing unit (CPU);

(b) a communication interface;

(c) a display device;

(d) an input device; and

(e) a database containing the polymorphism data;

wherein the polymorphism data comprises any one or more of the haplotypes set forth in the table immediately below:

HAPLOTYPE NUMBER[a]										PS[b]	PS
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	G	G	G	2	3409
A	A	A	A	A	A	A	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
A	A	A	A	A	A	A	G	G	G	5	4054
G	G	G	G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	A	G	G	8	12356
T	T	T	T	T	T	T	T	C	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	C	C	C	C	C	C	C	C	11	12653
A	G	G	G	G	G	G	G	G	G	12	14824
A	A	A	A	A	G	G	G	A	A	13	14990
C	C	C	C	T	C	C	C	C	C	14	15089
C	C	C	T	C	C	C	C	C	C	15	15093
C	C	T	C	C	C	T	T	T	C	16	15529
G	G	G	G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]										PS[b] NUMBER	PS POSITION[c]
11	12	13	14	15	16	17	18	19	20		
G	G	G	G	G	G	G	G	G	G	1	3102
G	G	G	G	G	G	G	T	T	T	2	3409
A	A	A	A	G	G	G	A	A	A	3	3438
C	C	C	C	C	C	C	C	C	C	4	3603
G	G	G	G	A	A	A	A	A	A	5	4054
G	G	G	G	G	G	G	A	G	G	6	4082
C	C	C	T	C	C	T	C	C	C	7	11998
G	G	G	G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	T	T	T	9	12397
C	C	C	C	C	C	C	C	C	C	10	12489
C	C	T	C	C	C	C	T	C	C	11	12653
G	G	G	G	G	G	G	G	G	G	12	14824
A	G	A	G	A	A	A	A	A	G	13	14990
C	C	C	C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	C	C	C	15	15093
T	T	T	T	C	T	C	T	T	T	16	15529
G	G	G	G	G	G	G	G	A	G	17	15932
G	G	G	G	G	G	G	G	G	G	18	16165

HAPLOTYPE NUMBER[a]							PS[b] NUMBER	PS POSITION[c]
21	22	23	24	25	26	27		
G	G	G	G	G	G	T	1	3102
T	T	T	T	T	T	G	2	3409
A	A	A	A	A	G	G	3	3438
C	C	C	C	G	C	C	4	3603
A	A	A	G	A	A	A	5	4054
G	G	G	G	G	G	G	6	4082
C	C	C	C	C	C	C	7	11998
G	G	G	G	G	G	G	8	12356
T	T	T	T	T	T	T	9	12397
C	C	T	C	C	C	C	10	12489
T	T	T	T	T	C	C	11	12653
G	G	G	G	G	G	G	12	14824
A	A	A	A	A	A	A	13	14990
C	C	C	C	C	C	C	14	15089
C	C	C	C	C	C	C	15	15093
C	T	T	T	T	C	T	16	15529
G	G	G	G	G	G	G	17	15932
G	G	G	G	G	G	A	18	16165

[a]Alleles for haplotypes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;

the haplotype pairs set forth in the table immediately below:

HAPLOTYPE PAIR[a]								PS[b]	PS
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	10	12489
C/C	T/T	C/C	T/C	C/C	C/C	T/T	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/19	3/14	12/15	22/8	2/9	3/21	2/15	12/17	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A	A/A	A/G	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	G/A	A/G	A/G	A/A	A/A	G/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/T	7	11998
G/G	G/G	G/G	G/A	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	C/C	C/C	T/C	C/C	C/T	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	12	14824
A/A	A/G	G/A	A/G	A/A	A/A	A/A	G/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/T	T/T	T/C	T/T	C/T	T/C	C/C	T/C	16	15529
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
C/C	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]								PS[b]	PS
3/27	22/10	2/16	2/26	22/11	12/7	22/2	22/18	NUMBER	POSITION[c]
G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/G	G/G	G/T	T/G	G/G	T/G	T/T	2	3409
A/G	A/A	A/G	A/G	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/A	A/G	A/A	A/A	A/G	G/A	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	6	4082
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	10	12489
C/C	T/C	C/C	C/C	T/C	C/C	T/C	T/T	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	A/A	A/A	G/G	A/A	A/A	13	14990
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	15	15093
T/T	T/C	C/T	C/C	T/T	T/T	T/C	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165

HAPLOTYPE PAIR[a]						PS[b]	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITION[c]
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	C/C	C/C	C/C	C/C	C/C	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	6	4082
C/C	C/C	C/C	C/C	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
C/C	C/C	C/C	C/C	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	C/C	C/C	C/C	C/C	14	15089
C/C	C/C	C/C	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

[a]Haplotype pairs are represented as 1st Haplotype/2nd Haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;
[c]Position of PS in SEQ ID NO:1;

and the frequency data in Tables 6 and 7.

34. A genome anthology for the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene which comprises two or more TNFRSF1A isogenes selected from the group consisting of isogenes 1-27 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
1	2	3	4	5	6	7	8	9	10	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	G	G	G	2	3409	1	2920-4210
A	A	A	A	A	A	A	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
A	A	A	A	A	A	A	G	G	G	5	4054	1	2920-4210
G	G	G	G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	A	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	C	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	C	C	C	C	C	C	C	C	11	12653	1	11417-12926
A	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	G	G	G	A	A	13	14990	1	14634-16768
C	C	C	T	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	T	C	C	C	C	C	C	15	15093	1	14634-16768
C	C	T	C	C	C	T	T	T	C	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]										PS[b]	PS	SEQ ID	REGION
11	12	13	14	15	16	17	18	19	20	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	G	G	G	G	1	3102	1	2920-4210
G	G	G	G	G	G	G	T	T	T	2	3409	1	2920-4210
A	A	A	A	G	G	G	A	A	A	3	3438	1	2920-4210
C	C	C	C	C	C	C	C	C	C	4	3603	1	2920-4210
G	G	G	G	A	A	A	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	A	G	G	6	4082	1	2920-4210
C	C	C	T	C	C	T	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	C	C	C	C	C	C	C	C	10	12489	1	11417-12926
C	C	T	C	C	C	C	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	G	G	G	12	14824	1	14634-16768
A	G	A	G	A	A	A	A	A	G	13	14990	1	14634-16768
C	C	C	C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	C	C	C	15	15093	1	14634-16768
T	T	T	T	C	T	C	T	T	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	G	A	G	17	15932	1	14634-16768
G	G	G	G	G	G	G	G	G	G	18	16165	1	14634-16768

ISOGENE NUMBER[a]							PS[b]	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION[c]	NO.	EXAMINED[d]
G	G	G	G	G	G	T	1	3102	1	2920-4210
T	T	T	T	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	C	C	C	G	C	C	4	3603	1	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	C	C	C	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	T	T	T	T	T	T	9	12397	1	11417-12926
C	C	T	C	C	C	C	10	12489	1	11417-12926
T	T	T	T	T	C	C	11	12653	1	11417-12926
G	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	C	C	C	C	C	C	15	15093	1	14634-16768
C	T	T	T	T	C	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	G	G	G	G	G	A	18	16165	1	14634-16768

[a]Alleles for isogenes are presented 5′ to 3′ in each column;
[b]PS = polymorphic site;
[c]Position of PS in SEQ ID NO:1;
[d]Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.